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engineering to produce specific fatty acids in significant quantities. Also, continuing to probe the substrate specificities of ALT-like enzymes from diverse plant species will lead to a greater understanding of their evolutionary origins and biological roles.

BI6. Metabolomics of resistant and susceptible potato genotypes reveals several resistance related metabolites involved in late blight resistance. S. Joshi[1*], A. Gagnon[2], A.C. Kushalappa[1] *[1]Department of Plant Science, McGill University, Ste.-Anne-de-Bellevue, Quebec, Canada [2]Progest2001 Inc. Marie-Victorin Sainte-Croix, Quebec, Canada*

Late blight of potato is a destructive disease caused by an oomycete, *Phytophthora infestans*. It has a worldwide occurrence, leading to yield loss of up to 40%. Managing the pathogen is still a difficult task. Resistance to late blight is either qualitative or quantitative. The quantitative resistance is durable, but the governing mechanisms are not completely deciphered, which limits its breeding applications. The objective of this study was to identify the resistance genes and their mechanisms, in a resistant genotype (Libertas) and a commercial susceptible genotype (AG704.10). These genotypes were grown in greenhouse, both leaves and stems were *P. infestans* or mock inoculated. Disease severity and pathogen biomass was monitored to quantify resistance. The late blight severity was assessed by measuring the lesion diameter overtime. The area under disease progress curve (AUDPC) was calculated using the lesion diameter and found to be significantly ($P < 0.01$) higher in AG704.10 (AUDPC = 177.97), as compared to Libertas (AUDPC = 96.69). The resistance related (RR) metabolites, with high fold change in resistant genotype compared to the susceptible, were identified. Several constitutively accumulated metabolites belonging to the flavonoid and alkaloid groups were found in Libertas. Also, key phenylpropanoids and flavonoids were found to be accumulated in Libertas leaves and stem post pathogen inoculation. These metabolites might be involved in late blight resistance. Moreover, the constitutive resistance appears to be the major mechanism imparting resistance in Libertas.

Concurrent Session V: Growth and Regulation

GR1. Deciphering species-specific pollen tube guidance in *Solanum*. V. Joly[1]*, C. Viallet[1], Y. Liu[1], A. Zaro[2], F. Ceriotti[3], D. P. Matton[1] *[1]Institut de Recherche en Biologie Végétale, Dép. de Sciences biologiques, Université de Montréal, Québec, Canada [2]Facultat de Biologia, Universitat de Barcelona, Catalonia, Spain [3]Laboratorio de Genómica Evolutiva, Grupo de Evolución Molecular de Plantas, Instituto de Biología Agrícola de Mendoza, CONICET-UNCuyo, Mendoza, Argentina.*

Small, secreted cysteine-rich proteins (CRPs) combine a highly stable cysteine spacing, ensuring conservation of their 3D structure and function, and hypervariable inter-cysteine blocks, allowing quick evolution of specific recognition domains. Interestingly, several CRPs were shown to control key pollen-pistil interactions in a species-specific way. The most emblematic example is perhaps the LURE defensin-like family, controlling directional guidance of pollen tubes (PTs) in *Torenia* and *Arabidopsis*.

We chose wild potatoes (*Solanum* sect. *Petota*) as a case study to investigate the impact of rapid CRP divergence in plant speciation. Gathering ~200 close species with overlapping distribution areas, this taxon indeed exhibits strong reproductive isolation. Lab-on-a-chip microfluidic experiments carried out on 4 species show that species-preferential PT attraction is a key factor in this isolation. We suspect polymorphic CRPs to control this attraction.

High-throughput sequencing technologies were applied to profile the ovule secretome as well as the reproductive transcriptomes of our 4 species of interest. To screen out candidate genes, we developped KAPPA, a sequence search algorithm specifically dedicated to CRPs, and obtained a set of 32 defensin-like groups expressed in ovules.

Five promising chemoattractant candidates exhibiting (i) ovule-specific expression, (ii) down-regulation in guidance-defective ovules, and (iii) interspecific divergence were selected for further characterization. They are currently being investigated with on-gel assays and specific microfluidic devices tailored for *Solanum* PTs. This study will lead to a better understanding of CRP-mediated PT chemoattraction as one of the

major species-specificity checkpoints that must be "unlocked" by pollen tubes in the pistil.

GR2. Investigating the role of autophagy in *Arabidopsis* self-incompatibility. H. Nelles[1]*, D.R. Goring[1,2]. [1]*Department of Cell and Systems Biology, University of Toronto and* [2]*Centre for the Analysis of Genome Evolution and Function, University of Toronto*

In the flowering plants, fertilization is controlled by a series of interactions between pollen and pistil. Members of the Brassicaceae have dry stigmas, allowing a plant to strictly regulate pollen acceptance through the selective hydration of compatible pollen grains. Most species within this family have acquired an outcrossing mechanism, known as self-incompatibility (SI), where self-pollen is rapidly rejected at the stigma surface. SI is achieved by disrupting the vesicular trafficking of stigmatic compatibility factors to the pollen contact site, thus preventing the germination of incompatible pollen. While the upstream SI signaling components, S cysteine-rich (SCR) and S-locus receptor kinase (SRK), have been characterized in *Arabidopsis lyrata*, the downstream signaling events require further investigation. In this study, we have transformed the inbreeding species *A. thaliana* with three genes from *A. lyrata* to establish a stable SI line. Stigmas from the SI line showed a specific rejection of self-pollen, resulting in a substantial reduction in seed set. We plan to further investigate the genetic requirements of SI and the putative role of autophagy in this mechanism. A GFP:ATG8 marker was introduced into SI lines and preliminary confocal work has revealed autophagosome formation in self-pollinated stigmatic papillae. The requirement for autophagy in SI will be further explored using autophagy T-DNA KO lines (*atg 5-1*, *atg7-2*) and by generating additional KO lines using CRISPR/Cas9 deletion.

GR3. Diversification of the histone acetyltransferase GCN5 through alternative splicing in *Brachypodium distachyon.* A. Martel[1*], H. Brar[1], B.F. Mayer[1], J.-B. Charron[1]. [1]*Department of Plant Science, McGill University, Macdonald Campus, Sainte-Anne-de-Bellevue, QC, Canada.*

The epigenetic modulatory SAGA complex is involved in various developmental and stress responsive pathways in plants. Alternative transcripts of the SAGA complex's enzymatic subunit GCN5 have been identified in *Brachypodium distachyon*. These splice variants differ based on the presence and integrity of their conserved domain sequences: the histone acetyltransferase domain, responsible for catalytic activity, and the bromodomain, involved in acetyl-lysine binding and genomic loci targeting. *GCN5* is the wild-type transcript, while alternative splice sites result in the transcriptional variants termed *L-GCN5* and *S-GCN5*. Absolute mRNA quantification revealed that, across eight *B. distachyon* accessions, *GCN5* was the dominant transcript isoform, followed by *L-GCN5* and *S-GCN5*. A cycloheximide treatment further revealed that the *S-GCN5* splice variant was degraded through the non-sense mediated decay pathway. All alternative *BdGCN5* transcripts displayed similar transcript profiles, being induced by heat and accumulating to higher levels in the crown, compared to aerial tissues. All predicted protein isoforms localize to the nucleus, corroborating their purported epigenetic functions. S-GCN5 was incapable of forming an *in vivo* protein interaction with ADA2, the transcriptional adaptor that links the histone acetyltransferase subunit to the SAGA complex, while both GCN5 and L-GCN5 interacted with ADA2. Therefore, a complete histone acetyltransferase domain is required for BdGCN5-BdADA2 interaction *in vivo*. Thus, there has been a diversification in *BdGCN5* through alternative splicing that result in differences in conserved domain composition, transcript fate and *in vivo* protein interaction partners. Furthermore, our results suggest that *B. distachyon* may harbor compositionally distinct SAGA-like complexes.

GR4. The possible role of SPL/miR156 module in controlling growth phase transition in barley. R.K. Tripathi*, J. Singh. *Dept. of Plant Science, McGill University, McGill University, Sainte Anne de Bellevue, QC, Canada.*

Barley, a major cereal grown worldwide, is self pollinating and diploid plant species. Plant